

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:02 ; Search time 29.37 Seconds

(without alignments)
30.788 Million cell updates/sec

Title: US-09-331-631A-32

Perfect score: 76
Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 28

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	74	1 M84B_DROME	001643 drosophila
2	67	88.2	55	1 M84C_DROME	001644 drosophila
3	67	88.2	56	1 AMCT_ADIME	P56882 apis mellif
4	67	88.2	57	1 MT2_SCYSE	P02806 scylla serr
5	67	88.2	58	1 MT1_HOMAM	P29499 homarus ame
6	67	88.2	58	1 MT1_SCYSE	P02805 scylla serr
7	67	88.2	58	1 MT2_CALSI	P55950 callinectes
8	67	88.2	58	1 MT_ASTRFL	P55951 astacus flu
9	67	88.2	58	1 MT_CARPA	P55948 caratus ma
10	67	88.2	58	1 MT_PORPO	P55952 callinectes
11	67	88.2	59	1 MT1_CALSI	P55949 callinectes
12	67	88.2	63	1 M84A_DROME	001642 drosophila
13	67	88.2	68	1 M84D_DROME	001645 drosophila
14	67	88.2	115	1 A62E_DROME	046202 drosophila
15	67	88.2	157	1 VES_RHPV1	P24834 rhesus papl
16	67	88.2	178	1 CHHC_HOMMO	P20730 bombyx mori
17	67	88.2	194	1 KRUH_HUMAN	O75690 homo sapien
18	67	88.2	247	1 ODEF_MOUSE	O61999 mus musculu
19	67	88.2	399	1 IGIR_MOUSE	O60751 mus musculu
20	67	88.2	728	1 KDCI_ARATH	O39017 arabidopsis
21	67	88.2	1133	1 RAD8_SCHPO	P36607 schizosach
22	67	88.2	1255	1 ERB2_HUMAN	P06426 homo sapien
23	67	88.2	1257	1 ERB2_RAT	P06494 ratus norv
24	67	88.2	1363	1 ILPR_BRALA	O02466 brachioosto
25	67	88.2	1367	1 IGIR_HUMAN	P08069 homo sapien
26	67	88.2	1370	1 IGIR_RAT	P24062 ratus norv
27	67	88.2	1372	1 INSR_MOUSE	P15708 mus musculu
28	67	88.2	1382	1 INSR_HUMAN	P06213 homo sapien
29	67	88.2	1383	1 INSR_RAT	P15127 ratus norv
30	67	88.2	2813	1 VWF_CANFA	O28295 canis famli
31	67	88.2	2813	1 VWF_HUMAN	P04275 homo sapien
32	66	86.8	71	1 MT21_MYTED	P80251 mytilus edu
33	66	86.8	71	1 MT22_MYTED	P80252 mytilus edu

34	66	86.8	71	1 MT23_MYTED	P80253 mytilus edu
35	66	86.8	72	1 MT11_MYTED	P80246 mytilus edu
36	66	86.8	72	1 MT12_MYTED	P80247 mytilus edu
37	66	86.8	72	1 MT13_MYTED	P80248 mytilus edu
38	66	86.8	72	1 MT14_MYTED	P80249 mytilus edu
39	66	86.8	95	1 KRFA_ANAPL	P08335 anas platyr
40	66	86.8	95	1 KRFA_COLLI	P07521 columba liv
41	66	86.8	97	1 KRFA_CHICK	P20308 gallus gall
42	66	86.8	97	1 KRFB_CHICK	P04458 gallus gall
43	66	86.8	97	1 KRFC_CHICK	P02450 gallus gall
44	66	86.8	97	1 KRFD_CHICK	P20307 gallus gall
45	66	86.8	98	1 KRFT_LARNO	P02451 larus novae

ALIGNMENTS

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RESULT 1
M84B_DROME          STANDARD;          PRT;          74 AA.
ID 001643;
AC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN MST84DB.
GN MST84DB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92102953; PubMed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
  Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
  of Drosophila melanogaster.";
RL Mech. Dev. 35:143-151(1991).
CC -!- TISSUE SPECIFICITY: TESTIS.
CC -!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -!- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
  MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC
DR EMBL: X67703; CAA47938.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004173; MST84DB.
KW Spermatogenesis; Repeat; Multigene family.
SQ
SEQUENCE 74 AA: 6824 MW: D0793137A/E7D1D0 CMC64;

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Query Match 100.0%; Score 76; DB 1; Length 74;
Best local similarity 21.4%; Pred. No. 5.2;
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXXC 28
DB 12 CSPGCGPCGCGPCGCGSCSPGSC 39

RESULT 2
M84C_DROME STANDARD; PRT; 55 AA.
ID 001644; Q9VIA0;


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RN [1]
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Larch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
2.";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
CC OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR; A03284; SMDZS.
DR HSSP; P55949; IDMF.
DR INTERPRO; IPRO02045; -.
DR INTERPRO; IPRO03019; -.
DR PRAM; PR00131; metalthio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28
FT METAL 29 57 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BAA3611 CRC64;
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Query Match 88.2%; Score 67; DB 1; Length 57;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CXXCXXCXXCXXCXXCXXCXXCXXCXX 27
DB 30 CECCSSGCKCANKEDCRKTCRKPCSC 56
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RESULT 5
MTL_HOMAM STANDARD; PRT; 58 AA.
AC P29499;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (CUMT-1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
RN [1]
RP SEQUENCE.
RX TISSUE=HEPATOPANCREAS;
RX MEDLINE=89215793; PubMed=2709004;
RA Brower M., Winge D.R., Gray W.R.;
RT "Structural and functional diversity of copper-metallothioneins from
the American lobster Homarus americanus.";
RL J. Inorg. Biochem. 35:289-303(1989).
RN [2]
RP STRUCTURE BY NMR.
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RX MEDLINE=94318629; PubMed=8043573;
RA Zhu Z., Derosé E.F., Mullen G.P., Petering D.H., Shaw C.F. III;
RT "Sequential proton resonance assignments and metal cluster topology
of lobster metallothionein-1.";
RL Biochemistry 33:8858-8865(1994).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF
CC LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.
CC CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION
CC OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN
CC TO BIND CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR; A37039; A37039.
DR HSSP; P55949; IDMF.
DR INTERPRO; IPRO02045; -.
DR INTERPRO; IPRO03019; -.
DR PRAM; PR00131; metalthio; 1.
DR PRINTS; PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 28
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 5975 MW; 176ABA6F60A32F96 CRC64;
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Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CXXCXXCXXCXXCXXCXXCXXCXXCXX 27
DB 30 CERCTSGCKCPKDECAKTCRKPCSC 56
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RESULT 6
MTL_SCYSE STANDARD; PRT; 58 AA.
AC P02805;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-1 (MT-1).
OS Scylla serrata (Mud crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Scylla.
RN [1]
RP SEQUENCE.
RX MEDLINE=82142340; PubMed=7061431;
RA Larch K., Ammer D., Olafson R.W.;
RT "Crab metallothionein. Primary structures of metallothioneins 1 and
2.";
RL J. Biol. Chem. 257:2420-2426(1982).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
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OF HEAVY-METAL IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR: A03283; SMKDIS.
DR HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 28 BETA.
FT METAL 29 58 ALPHA.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 9 9 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER A.
FT METAL 33 33 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 39 39 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 53 53 CLUSTER A.
FT METAL 55 55 CLUSTER A.
FT METAL 56 56 CLUSTER A.
SQ SEQUENCE 58 AA; 6001 MW; CE8A24C590B027B8 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXXCXXXXXXCXXXXX 27
DB 30 CCKCSGCKCANKECKSKTCSKACSCC 56

RESULT 7
MT2_CALSI
ID MT2_CALSI STANDARD: PRT; 58 AA.
AC P55950;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunidea; Portunidae; Callinectes.
RN [1]
RP SEQUENCE.
RX MEDLINE-96033062; PubMed-7487904;
RA Browner M., Enghild J., Hoexum-Brouwer T., Thogersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
(Callinectes sapidus) metallothionein isoforms.";
RL Biochem. J. 311:617-622(1995).
CC -1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CC CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.

FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
SQ SEQUENCE 58 AA; 6287 MW; EF679CB94975C5F0 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXXCXXXXXXCXXXXX 27
DB 31 CCKCSGCKCTSKCKSKTCSKPCSCC 57

RESULT 8
MT_ASTFL
ID MT_ASTFL STANDARD: PRT; 58 AA.
AC P55951;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Astacus fluviatilis (Broad-fingered crayfish) (Astacus astacus).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacidea; Astacidae; Astacus.
RN [1]
RP SEQUENCE.
RX TISSUE-MIDGUT;
MEDLINE-97079279; PubMed-8921011;
RA Pedersen S.N., Pedersen K.L., Hoerjrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:999-1003(1996).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
CC ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
CC METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MW=5910.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
CC HSSP: P55949; 1DMF.
DR INTERPRO: IPR002045; -.
DR INTERPRO: IPR003019; -.
DR PFAM: PF00131; metalchio.1.
DR PRINTS: PR00858; MTCRUSTACEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 BETA.
FT METAL 30 58 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.

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FT METAL 31 31 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
SEQUENCE 58 AA; 5911 MW; 576365B3BE5C7122 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXX 27
D 31 CDKCTSGCKCPKCECAKTCCKPCECC 57

RESULT 9
ID MT_CARMA STANDARD; PRT; 58 AA.
AC P55948;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC TISSUE=MIDGUT; PubMed=8110201;
RA Pedersen K.L., Pedersen S.N., Hoefjrup P., Andersen J.S.,
RA Reepstorff P., Knudsen J., Depledge M.H.;
RT "Purification and characterization of a cadmium-induced
metallothionein from the shore crab Carcinus maenas (L.).";
RL Biochem. J. 297:609-614(1994).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
OF HEAVY-METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP; P55949; IDMD.
DR INTERPRO: IPR002045; -.
DR PRAM: PF00131; metalthio. 1.
DR PRINTS: PR00856; MTCRUSTACEAN.
KW Metal-binding; Metal-chiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER B.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.

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FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT VARIANT 1 1 MISSING (IN VARIANT ISOLATED IN LOW
SEQUENCE 58 AA; 6133 MW; 0167CDA2E9C9731D CRC64;

Query Match 88.2%; Score 67; DB 1; Length 58;
Best Local Similarity 18.5%; Pred. No. 23;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXX 27
D 31 CEKSSGCKCTTKEDCKCTCKPSCC 57

RESULT 10
ID MT_POTPO STANDARD; PRT; 58 AA.
AC P55952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN (MT).
OS Potamon potamios.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Geiryonidae; Potamon.
RN [1]
RP SEQUENCE.
RC TISSUE=MIDGUT; PubMed=8921011;
RA Pedersen S.N., Pedersen K.L., Hoefjrup P., Depledge M.H., Knudsen J.;
RT "Primary structures of decapod crustacean metallothioneins with
special emphasis on freshwater and semi-terrestrial species.";
RL Biochem. J. 319:999-1003(1996).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-
METAL IONS.
CC -1- INDUCTION: BY CADMIUM.
CC -1- MASS SPECTROMETRY: MW=6156.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR HSSP; P55949; IDMD.
DR INTERPRO: IPR002045; -.
DR PRAM: PF00131; metalthio. 1.
DR PRINTS: PR00856; MTCRUSTACEAN.
KW Metal-binding; Metal-chiolate cluster; Chelation; Cadmium.
FT DOMAIN 1 29 ALPHA.
FT METAL 30 58 CLUSTER B.
FT METAL 4 4 CLUSTER B.
FT METAL 5 5 CLUSTER B.
FT METAL 10 10 CLUSTER B.
FT METAL 12 12 CLUSTER B.
FT METAL 17 17 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 23 23 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 28 28 CLUSTER B.
FT METAL 31 31 CLUSTER B.
FT METAL 34 34 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 40 40 CLUSTER A.
FT METAL 46 46 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 54 54 CLUSTER A.
FT METAL 56 56 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT METAL 58 58 CLUSTER A.

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[illegible]

Query	1	CXXCXXCXXXXXXXXXXCXXCXX	27
Best Match	1	: : : :	
Local Similarity	31	CÖKCTSGCKATKEBCSKTCTKPCSCC	57
Matches		5; Conservative	22; Mismatches
			0; Indels
			0; Gaps

	RESULT	11		
ID	MTL_CALSI		PRT:	59 AA.
AC	p55949;	STANDARD;		
DT	01-NOV-1997 (Rel. 35,	Created)		
DT	01-NOV-1997 (Rel. 35,	Last sequence update)		
DE	METALLOTHIONEIN-I (M-TI) (M-TB/M-TIA).			
OS	Callinectes sapidus (Blue crab).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
CC	Eumalacostrata; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eubrachyura; Portunoidae; Portunidae; Callinectes.			
RN	[1]			
RP	SEQUENCE.			
RA	BROWDER M., Engbild J., Hoxeum-Brouwer T., Thøgersen I., Truncali A.;			
RT	"Primary structure and tissue-specific expression of blue crab			
RL	(<i>Callinectes sapidus</i>) metalllothionein isoforms."			
RB	Biochem. J. 311:617-622(1995).			
RN	[2]			
RP	STRUCTURE BY NMR.			
RA	NERULA S.S., Brouwer M., Hua Y., Armillage L.M.;			
RT	"Three-dimensional solution structure of <i>Callinectes sapidus</i>			
RL	metallothionein-I determined by homonuclear and heteronuclear			
RB	magnetic resonance spectroscopy."			
RL	Biochemistry 34:620-631(1995).			
CC	-1- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND CADMIUM.			
CC	CADMIUM.			
DR	-1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.			
DR	PDB; IDMC; 07-FEB--95.			
DR	PDB; IDMED; 07-FEB--95.			
DR	PDB; IDMF; 07-FEB--95.			
DR	INTERPRO: IPRO02045; -			
DR	INTERPRO: IPRO03019; -			
DR	PPAM; PP00131; metalthio. 1.			
DR	PRINTS; PR00855; MTCRUSTACEAN.			
KW	Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium;			
KW	3D-structure.			
FT	DOMAIN	1	29	BETA.
FT		30	59	ALPHA.
FT	METAL	5	5	CLUSTER B.
FT	METAL	6	6	CLUSTER B.
FT	METAL	10	10	CLUSTER B.
FT	METAL	12	12	CLUSTER B.
FT	METAL	17	17	CLUSTER B.
FT	METAL	21	21	CLUSTER B.
FT	METAL	23	23	CLUSTER B.
FT	METAL	26	26	CLUSTER B.
FT	METAL	28	28	CLUSTER B.
FT	METAL	31	31	CLUSTER A.
FT	METAL	34	34	CLUSTER A.
FT	METAL	38	38	CLUSTER A.
FT	METAL	40	40	CLUSTER A.
FT	METAL	46	46	CLUSTER A.
FT	METAL	50	50	CLUSTER A.
FT	METAL	54	54	CLUSTER A.
FT	METAL	56	56	CLUSTER A.
FT	METAL	57	57	CLUSTER A.
FT	VARIANT	1	1	MISSING (IN MT-IA).
SQ	SEQUENCE	59 AA;	6141 MM;	439BD0A9DIAG6034 CRC64;

RESULT	12
MS44_DROME	
ID	MS44_DROME
AC	001642; 09VITA3;
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	MALE SPECIFIC SPERM PROTEIN MS184DA.
CN	MS184DA.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=OREGON-R;
RX	MEDLINE=92102953; PubMed=1684716;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Mananalis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abell J.F., Agapayni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Bailly R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bernick B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davis A.P., Davies P., Harris M.,
RA	de Pablos R., Delcher A., Deng Z., Meyers A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harits N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibergam C.,
RA	Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merklou G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paetle J.M.,
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Styrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT	"The genome sequence of Drosophila melanogaster."
RL	Science 287:2185-2195 (2000).

```

CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X67703; CAA47937.1; -.
DR EMBL: AE003672; AAF54022.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004172; Mst84Da.
KM Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 63 AA; 5806 MW; BF84CD74CBCEFD3F CRC64;

Query Match 88.2%; Score 67; DB 1; Length 63;
Best Local Similarity 18.5%; Pred. No. 24;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 2 XXXXXXXXXX XXXXXXXXXX XXXXXXXX 28
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 14 GPCGCGCGCGCGCGCGCGCGCGCGCGC 40

RESULT 13
M84D_DROME STANDARD; PRT; 68 AA.
AC 001645;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MALE SPECIFIC SPERM PROTEIN MSTR84D.
GN MSTR84D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RX MEDLINE=92102953; PubMed=1684716;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA Schaefer M.,
RT A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster.*;
RL Mech. Dev. 35:143-151(1991).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
CC -1- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
CC MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X67703; CAA47940.1; -.
DR HSSP: P01180; INPO.
DR FLYBASE: FBgn0004175; Mst84Dd.
KM Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 68 AA; 6480 MW; 2F2BD26128DE3DDE CRC64;

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Query Match 88.2%; Score 67; DB 1; Length 68;
Best Local Similarity 18.5%; Pred. No. 26;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXCXXXXXXX XXXXXXXXXX XXXXXXXX 27
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 13 GPCGCGCGCGCGCGCGCGCGCGCGC 39

RESULT 14
A62F_DROME STANDARD; PRT; 115 AA.
AC 046202;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ACCESSORY GLAND PROTEIN ACP62F.
GN ACP62F.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S; TISSUE=MALE ACCESSORY GLAND;
RX MEDLINE=98135120; PubMed=9474779;
RA Wolfner M.F., Harada H.A., Bertram M.J., Stelick T.J., Kraus K.W.,
RA Kalb J.M., Lung Y.O., Neubaum D.M., Park M., Tiam U.;
RT "New genes for male accessory gland proteins in Drosophila
RT melanogaster."
RL Insect Biochem. Mol. Biol. 27:825-834(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abrial J.F., Adhayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervio G., Milshina N.V., Modarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitsks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

```

Search completed: March 1, 2001, 16:26:02
Job time: 399 sec

RL Science 287:2185-2195(2000).
CC -1- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES IN
CC MATED FEMALE FLIES.
CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -----
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CC -----
CC EMBL: U85763; AAB96387.1; -.
DR EMBL: AE003475; AAF47683.1; -.
DR FLYBASE: FBgn020509; ACP62F.
KW Behavior.
SQ SEQUENCE 115 AA; 12570 MW; 4326AA6FC32291D CRC64;

Query Match 88.2%; Score 67; DB 1; Length 115;
Best Local Similarity 18.5%; Pred. No. 37;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXXXXXXXXX
DB 41 TECPVACPETCEXGNGPCVKMGAPC 67

RESULT 15

VE5_RHPV1 STANDARD; PRT; 157 AA.
AC P24834;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PROBABLE E5 PROTEIN.
GN E5.
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135018; PubMed-1847267;
RA Ostrow R.S., Labresh K.V., Farias A.J.;
RT "Characterization of the complete Rhpv 1 genomic sequence and an
RT integration locus from a metastatic tumor."
RL Virology 181:424-429(1991).
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CC -----
CC EMBL: M60184; AAA79315.1; ALT_SEQ.
DR EMBL: M60184; AAA79316.1; ALT_SEQ.
DR PIR: F38503; W5WLR1.
KW Early protein.
SQ SEQUENCE 157 AA; 17398 MW; AC7AA67158844686 CRC64;

Query Match 88.2%; Score 67; DB 1; Length 157;
Best Local Similarity 18.5%; Pred. No. 46;
Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXXXXXXXXX
DB 23 VLCKANCCCYACKPPFCFCWLCFCCC 49